Sergio Baranzini

List of Publications by Year in Descending Order

180 papers	15,808 citations	53 h-index	125 g-index
206 ext. papers	19,126 ext. citations	9.9 avg, IF	6.25 L-index

#	Paper	IF	Citations
180	A biomedical open knowledge network harnesses the power of AI to understand deep human biology. *AI Magazine*, **2022**, 43, 46-58	6.1	1
179	MRI-derived g-ratio and lesion severity in newly diagnosed multiple sclerosis. *Brain Communications* , **2021**, 3, fcab249	4.5	1
178	Embedding electronic health records onto a knowledge network recognizes prodromal features of multiple sclerosis and predicts diagnosis.. *Journal of the American Medical Informatics Association: JAMIA*, **2021**,	8.6	4
177	Cell type-specific transcriptomics identifies neddylation as a novel therapeutic target in multiple sclerosis. *Brain*, **2021**, 144, 450-461	11.2	5
176	Childhood obesity and multiple sclerosis: A Mendelian randomization study. *Multiple Sclerosis Journal*, **2021**, 27, 2150-2158	5	8
175	Classification of neurological diseases using multi-dimensional CSF analysis. *Brain*, **2021**, 144, 2625-2634	11.2	6
174	Distinctive waves of innate immune response in the retina in experimental autoimmune encephalomyelitis. *JCI Insight*, **2021**, 6,	9.9	4
173	Mendelian randomization study shows no causal effects of serum urate levels on the risk of MS. *Neurology: Neuroimmunology and NeuroInflammation*, **2021**, 8,	9.1	2
172	Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases. *Life*, **2021**, 11,	3	4
171	The relative contributions of obesity, vitamin D, leptin, and adiponectin to multiple sclerosis risk: A Mendelian randomization mediation analysis. *Multiple Sclerosis Journal*, **2021**, 27, 1994-2000	5	4
170	Specific hypomethylation programs underpin B cell activation in early multiple sclerosis.. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	2
169	Levels of brain-derived neurotrophic factor in patients with multiple sclerosis. *Annals of Clinical and Translational Neurology*, **2020**, 7, 2251-2261	5.3	4
168	Vitamin D Regulates MerTK-Dependent Phagocytosis in Human Myeloid Cells. *Journal of Immunology*, **2020**, 205, 398-406	5.3	4
167	Serum antibodies to phosphatidylcholine in MS. *Neurology: Neuroimmunology and NeuroInflammation*, **2020**, 7,	9.1	3
166	microRNA and exosome profiling in multiple sclerosis. *Multiple Sclerosis Journal*, **2020**, 26, 599-604	5	13
165	SARS-CoV-2 meta-interactome suggests disease-specific, autoimmune pathophysiologies and therapeutic targets. *F1000Research*, **2020**, 9, 992	3.6	5
164	Gut microbiota-specific IgA B cells traffic to the CNS in active multiple sclerosis. *Science Immunology* , **2020**, 5,	28	48

163	A pathogenic and clonally expanded B cell transcriptome in active multiple sclerosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 22932-22943	11.5	43
162	Household paired design reduces variance and increases power in multi-city gut microbiome study in multiple sclerosis. *Multiple Sclerosis Journal*, **2020**, 1352458520924594	5	5
161	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. *Science*, **2019**, 365,	33.3	309
160	Insights into microbiome research 4: The computational analysis. *Multiple Sclerosis Journal*, **2019**, 25, 21-22	5	
159	Selective Estrogen Receptor Modulators Enhance CNS Remyelination Independent of Estrogen Receptors. *Journal of Neuroscience*, **2019**, 39, 2184-2194	6.6	24
158	Insights into microbiome research 5: Mapping is first but function must come next. *Multiple Sclerosis Journal*, **2019**, 25, 193-195	5	
157	Aberrant oligodendroglial-vascular interactions disrupt the blood-brain barrier, triggering CNS inflammation. *Nature Neuroscience*, **2019**, 22, 709-718	25.5	61
156	Silent progression in disease activity-free relapsing multiple sclerosis. *Annals of Neurology*, **2019**, 85, 653-666	9.4	135
155	Insights into microbiome research 6: The role of consortia in studying the role of microbes in health and disease. *Multiple Sclerosis Journal*, **2019**, 25, 336-337	5	2
154	Integrating biomedical research and electronic health records to create knowledge-based biologically meaningful machine-readable embeddings. *Nature Communications*, **2019**, 10, 3045	17.4	20
153	Early complement genes are associated with visual system degeneration in multiple sclerosis. *Brain*, **2019**, 142, 2722-2736	11.2	13
152	Genetic variation across RNA metabolism and cell death gene networks is implicated in the semantic variant of primary progressive aphasia. *Scientific Reports*, **2019**, 9, 10854	4.9	5
151	Disease-modifying therapies alter gut microbial composition in MS. *Neurology: Neuroimmunology and NeuroInflammation*, **2019**, 6, e517	9.1	43
150	Recirculating Intestinal IgA-Producing Cells Regulate Neuroinflammation via IL-10. *Cell*, **2019**, 176, 610-624.e18	36.2	133
149	Harnessing electronic medical records to advance research on multiple sclerosis. *Multiple Sclerosis Journal*, **2019**, 25, 408-418	5	15
148	The microbiome and MS: The influence of the microbiota on MS risk and progression-Session chair summary. *Multiple Sclerosis Journal*, **2018**, 24, 587-589	5	0
147	The Gut Microbiome in Neuromyelitis Optica. *Neurotherapeutics*, **2018**, 15, 92-101	6.4	31
146	The era of GWAS is over - Commentary. *Multiple Sclerosis Journal*, **2018**, 24, 260-261	5	

145	Multiple sclerosis. *Lancet, The*, **2018**, 391, 1622-1636	40	698
144	Mononuclear cell transcriptome changes associated with dimethyl fumarate in MS. *Neurology: Neuroimmunology and NeuroInflammation*, **2018**, 5, e470	9.1	4
143	Insights into microbiome research 1: How to choose appropriate controls for a microbiome study in MS?. *Multiple Sclerosis Journal*, **2018**, 24, 1278-1279	5	3
142	Genome sequencing uncovers phenocopies in primary progressive multiple sclerosis. *Annals of Neurology*, **2018**, 84, 51-63	9.4	21
141	The Role of the Gut Microbiome in Multiple Sclerosis Risk and Progression: Towards Characterization of the "MS Microbiome". *Neurotherapeutics*, **2018**, 15, 126-134	6.4	39
140	Multiple Sclerosis-Associated Changes in the Composition and Immune Functions of Spore-Forming Bacteria. *MSystems*, **2018**, 3,	7.6	36
139	Insights into microbiome research 2: Experimental design, sample collection, and shipment. *Multiple Sclerosis Journal*, **2018**, 24, 1419-1420	5	4
138	Protein network analysis reveals selectively vulnerable regions and biological processes in FTD. *Neurology: Genetics*, **2018**, 4, e266	3.8	7
137	Insights into microbiome research 3: Who's there versus what are they doing?. *Multiple Sclerosis Journal*, **2018**, 24, 1541-1542	5	
136	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. *Cell*, **2018**, 175, 1679-1687.e7	38.2	72
135	The autoimmune risk gene ZMIZ1 is a vitamin D responsive marker of a molecular phenotype of multiple sclerosis. *Journal of Autoimmunity*, **2017**, 78, 57-69	15.5	18
134	Data characterizing the ZMIZ1 molecular phenotype of multiple sclerosis. *Data in Brief*, **2017**, 11, 364-370	1.2	3
133	The Genetics of Multiple Sclerosis: From 0 to 200 in 50 Years. *Trends in Genetics*, **2017**, 33, 960-970	8.5	103
132	Gut microbiota from multiple sclerosis patients enables spontaneous autoimmune encephalomyelitis in mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 10719-10724	11.5	441
131	Gut bacteria from multiple sclerosis patients modulate human T cells and exacerbate symptoms in mouse models. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 10713-10718	11.5	453
130	IFN-□rchestrates mesenchymal stem cell plasticity through the signal transducer and activator of transcription 1 and 3 and mammalian target of rapamycin pathways. *Journal of Allergy and Clinical Immunology*, **2017**, 139, 1667-1676	11.5	31
129	Systematic integration of biomedical knowledge prioritizes drugs for repurposing. *ELife*, **2017**, 6,	8.9	151
128	Long-term evolution of multiple sclerosis disability in the treatment era. *Annals of Neurology*, **2016**, 80, 499-510	9.4	229

127	Gut microbiome analysis in neuromyelitis optica reveals overabundance of Clostridium perfringens. *Annals of Neurology*, **2016**, 80, 443-7	9.4	95
126	NR1H3 p.Arg415Gln Is Not Associated to Multiple Sclerosis Risk. *Neuron*, **2016**, 92, 333-335	13.9	19
125	Association of HLA Genetic Risk Burden With Disease Phenotypes in Multiple Sclerosis. *JAMA Neurology*, **2016**, 73, 795-802	17.2	43
124	Immune cell-specific transcriptional profiling highlights distinct molecular pathways controlled by Tob1 upon experimental autoimmune encephalomyelitis. *Scientific Reports*, **2016**, 6, 31603	4.9	7
123	Meta-analysis of genome-wide association studies reveals genetic overlap between Hodgkin lymphoma and multiple sclerosis. *International Journal of Epidemiology*, **2016**, 45, 728-40	7.8	16
122	Genetic associations with brain cortical thickness in multiple sclerosis. *Genes, Brain and Behavior*, **2015**, 14, 217-27	3.6	25
121	SNP imputation bias reduces effect size determination. *Frontiers in Genetics*, **2015**, 6, 30	4.5	4
120	Whole genome sequences of 2 octogenarians with sustained cognitive abilities. *Neurobiology of Aging*, **2015**, 36, 1435-8	5.6	1
119	A robust type I interferon gene signature from blood RNA defines quantitative but not qualitative differences between three major IFN drugs in the treatment of multiple sclerosis. *Human Molecular Genetics*, **2015**, 24, 3192-205	5.6	7
118	A non-synonymous single-nucleotide polymorphism associated with multiple sclerosis risk affects the EVI5 interactome. *Human Molecular Genetics*, **2015**, 24, 7151-8	5.6	14
117	Genetic contribution to multiple sclerosis risk among Ashkenazi Jews. *BMC Medical Genetics*, **2015**, 16, 55	2.1	7
116	Class II HLA interactions modulate genetic risk for multiple sclerosis. *Nature Genetics*, **2015**, 47, 1107-1113	36.3	215
115	A validated gene regulatory network and GWAS identifies early regulators of T cell-associated diseases. *Science Translational Medicine*, **2015**, 7, 313ra178	17.5	45
114	Interferon-beta affects mitochondrial activity in CD4+ lymphocytes: Implications for mechanism of action in multiple sclerosis. *Multiple Sclerosis Journal*, **2015**, 21, 1262-70	5	7
113	Prognostic biomarkers of IFNb therapy in multiple sclerosis patients. *Multiple Sclerosis Journal*, **2015**, 21, 894-904	5	13
112	PINBPA: cytoscape app for network analysis of GWAS data. *Bioinformatics*, **2015**, 31, 262-4	7.2	25
111	ID: 144. *Cytokine*, **2015**, 76, 93	4	
110	Assessing the Power of Exome Chips. *PLoS ONE*, **2015**, 10, e0139642	3.7	6

109	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. *F1000Research*, **2015**, 4, 485	3.6	7
108	iCTNet2: integrating heterogeneous biological interactions to understand complex traits. *F1000Research*, **2015**, 4, 485	3.6	6
107	Heterogeneous Network Edge Prediction: A Data Integration Approach to Prioritize Disease-Associated Genes. *PLoS Computational Biology*, **2015**, 11, e1004259	5	69
106	Renaming "heterogeneous networks" to a more concise and catchy term **2015**,		2
105	iPINBPA: an integrative network-based functional module discovery tool for genome-wide association studies. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2015**, 255-66	1.3	8
104	Parallel states of pathological Wnt signaling in neonatal brain injury and colon cancer. *Nature Neuroscience*, **2014**, 17, 506-12	25.5	76
103	Astrocyte-encoded positional cues maintain sensorimotor circuit integrity. *Nature*, **2014**, 509, 189-94	50.4	202
102	A gene pathway analysis highlights the role of cellular adhesion molecules in multiple sclerosis susceptibility. *Genes and Immunity*, **2014**, 15, 126-32	4.4	23
101	Rituximab efficiently depletes increased CD20-expressing T cells in multiple sclerosis patients. *Journal of Immunology*, **2014**, 193, 580-586	5.3	160
100	Precision medicine in chronic disease management: The multiple sclerosis BioScreen. *Annals of Neurology*, **2014**, 76, 633-42	9.4	36
99	The autoimmune disease-associated transcription factors EOMES and TBX21 are dysregulated in multiple sclerosis and define a molecular subtype of disease. *Clinical Immunology*, **2014**, 151, 16-24	9	37
98	Blood miRNA expression pattern is a possible risk marker for natalizumab-associated progressive multifocal leukoencephalopathy in multiple sclerosis patients. *Multiple Sclerosis Journal*, **2014**, 20, 1851-9	5	43
97	Modules, networks and systems medicine for understanding disease and aiding diagnosis. *Genome Medicine*, **2014**, 6, 82	14.4	126
96	Naive CD4 T-cell activation identifies MS patients having rapid transition to progressive MS. *Neurology*, **2014**, 82, 681-90	6.5	17
95	The role of antiproliferative gene Tob1 in the immune system. *Clinical and Experimental Neuroimmunology*, **2014**, 5, 132-136	0.4	16
94	Meta-Analysis of Hodgkin Lymphoma and Asthma Genome-Wide Association Scans reveals common variants in GATA3. *Blood*, **2014**, 124, 135-135	2.2	
93	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
92	A genome-wide association study of brain lesion distribution in multiple sclerosis. *Brain*, **2013**, 136, 1012-24	10.2	45

91	Blood RNA profiling in a large cohort of multiple sclerosis patients and healthy controls. *Human Molecular Genetics*, **2013**, 22, 4194-205	5.6	58
90	Sequencing of the IL6 gene in a case-control study of cerebral palsy in children. *BMC Medical Genetics*, **2013**, 14, 126	2.1	15
89	Hippocampal demyelination and memory dysfunction are associated with increased levels of the neuronal microRNA miR-124 and reduced AMPA receptors. *Annals of Neurology*, **2013**, 73, 637-45	9.4	117
88	Tob1 plays a critical role in the activation of encephalitogenic T cells in CNS autoimmunity. *Journal of Experimental Medicine*, **2013**, 210, 1301-9	16.6	32
87	Expression profiling of Aldh1l1-precursors in the developing spinal cord reveals glial lineage-specific genes and direct Sox9-Nfe2l1 interactions. *Glia*, **2013**, 61, 1518-32	9	41
86	Autoimmune Disorders **2013**, 822-838		3
85	Opposite roles of NMDA receptors in relapsing and primary progressive multiple sclerosis. *PLoS ONE*, **2013**, 8, e67357	3.7	25
84	The genetics of multiple sclerosis: an up-to-date review. *Immunological Reviews*, **2012**, 248, 87-103	11.3	192
83	Data integration and systems biology approaches for biomarker discovery: challenges and opportunities for multiple sclerosis. *Journal of Neuroimmunology*, **2012**, 248, 58-65	3.5	32
82	Detection of identity by descent using next-generation whole genome sequencing data. *BMC Bioinformatics*, **2012**, 13, 121	3.6	16
81	In depth comparison of an individual's DNA and its lymphoblastoid cell line using whole genome sequencing. *BMC Genomics*, **2012**, 13, 477	4.5	29
80	Transcriptional expression patterns triggered by chemically distinct neuroprotective molecules. *Neuroscience*, **2012**, 226, 10-20	3.9	4
79	Genetics of multiple sclerosis: swimming in an ocean of data. *Current Opinion in Neurology*, **2012**, 25, 239-45	7.1	40
78	Janus-like opposing roles of CD47 in autoimmune brain inflammation in humans and mice. *Journal of Experimental Medicine*, **2012**, 209, 1325-34	16.6	108
77	Axin2 as regulatory and therapeutic target in newborn brain injury and remyelination. *Nature Neuroscience*, **2011**, 14, 1009-16	25.5	265
76	Modeling the cumulative genetic risk for multiple sclerosis from genome-wide association data. *Genome Medicine*, **2011**, 3, 3	14.4	48
75	Myelin regeneration: a recapitulation of development?. *Annual Review of Neuroscience*, **2011**, 34, 21-43	17	242
74	Revealing the genetic basis of multiple sclerosis: are we there yet?. *Current Opinion in Genetics and Development*, **2011**, 21, 317-24	4.9	44

73	Manitoba-oculo-tricho-anal (MOTA) syndrome is caused by mutations in FREM1. *Journal of Medical Genetics*, **2011**, 48, 375-82	5.8	46
72	Functional energetics of CD4+-cellular immunity in monoclonal antibody-associated progressive multifocal leukoencephalopathy in autoimmune disorders. *PLoS ONE*, **2011**, 6, e18506	3.7	19
71	iCTNet: a Cytoscape plugin to produce and analyze integrative complex traits networks. *BMC Bioinformatics*, **2011**, 12, 380	3.6	30
70	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
69	Genome, epigenome and RNA sequences of monozygotic twins discordant for multiple sclerosis. *Nature*, **2010**, 464, 1351-6	50.4	390
68	Genetic variation influences glutamate concentrations in brains of patients with multiple sclerosis. *Brain*, **2010**, 133, 2603-11	11.2	107
67	Multiple sclerosis genetics--is the glass half full, or half empty?. *Nature Reviews Neurology*, **2010**, 6, 429-37	7.5	103
66	Genetic variation in the odorant receptors family 13 and the mhc loci influence mate selection in a multiple sclerosis dataset. *BMC Genomics*, **2010**, 11, 626	4.5	13
65	Incidental MRI anomalies suggestive of multiple sclerosis: the radiologically isolated syndrome. *Neurology*, **2009**, 72, 800-5	6.5	361
64	Pathway and network-based analysis of genome-wide association studies in multiple sclerosis. *Human Molecular Genetics*, **2009**, 18, 2078-90	5.6	310
63	Genotype-Phenotype correlations in multiple sclerosis: HLA genes influence disease severity inferred by 1HMR spectroscopy and MRI measures. *Brain*, **2009**, 132, 250-9	11.2	132
62	Longitudinal system-based analysis of transcriptional responses to type I interferons. *Physiological Genomics*, **2009**, 38, 362-71	3.6	25
61	Dysregulation of the Wnt pathway inhibits timely myelination and remyelination in the mammalian CNS. *Genes and Development*, **2009**, 23, 1571-85	12.6	459
60	Changes in matrix metalloproteinases and their inhibitors during interferon-beta treatment in multiple sclerosis. *Clinical Immunology*, **2009**, 130, 145-50	9	36
59	Systems biology and its application to the understanding of neurological diseases. *Annals of Neurology*, **2009**, 65, 124-39	9.4	82
58	The genetics of autoimmune diseases: a networked perspective. *Current Opinion in Immunology*, **2009**, 21, 596-605	7.8	110
57	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. *Nature Genetics*, **2009**, 41, 776-82	36.3	621
56	Genome-wide association analysis of susceptibility and clinical phenotype in multiple sclerosis. *Human Molecular Genetics*, **2009**, 18, 767-78	5.6	357

55	Differential micro RNA expression in PBMC from multiple sclerosis patients. *PLoS ONE*, **2009**, 4, e6309	3.7	184
54	Proteomic analysis of active multiple sclerosis lesions reveals therapeutic targets. *Nature*, **2008**, 451, 1076-81	50.4	406
53	The genetics of multiple sclerosis: SNPs to pathways to pathogenesis. *Nature Reviews Genetics*, **2008**, 9, 516-26	30.1	259
52	Genome-wide pharmacogenomic analysis of the response to interferon beta therapy in multiple sclerosis. *Archives of Neurology*, **2008**, 65, 337-44		135
51	Abrogation of T cell quiescence characterizes patients at high risk for multiple sclerosis after the initial neurological event. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 11839-44	11.5	83
50	Uncoupling the roles of HLA-DRB1 and HLA-DRB5 genes in multiple sclerosis. *Journal of Immunology*, **2008**, 181, 5473-80	5.3	83
49	Evidence for association of chromosome 10 open reading frame (C10orf27) gene polymorphisms and multiple sclerosis. *Multiple Sclerosis Journal*, **2008**, 14, 412-4	5	5
48	A framework and mechanistically focused, in silico method for enabling rational translational research. *Summit on Translational Bioinformatics*, **2008**, 2008, 46-50		
47	Gene expression profiling in neurological and neuroinflammatory diseases **2008**, 115-130		1
46	Quantitative longitudinal analysis of T cell receptor repertoire expression in HIV-infected patients on antiretroviral and interleukin-2 therapy. *AIDS Research and Human Retroviruses*, **2007**, 23, 741-7	1.6	5
45	Genome-wide network analysis reveals the global properties of IFN-beta immediate transcriptional effects in humans. *Journal of Immunology*, **2007**, 178, 5076-85	5.3	39
44	The molecular signature of therapeutic mesenchymal stem cells exposes the architecture of the hematopoietic stem cell niche synapse. *BMC Genomics*, **2007**, 8, 65	4.5	53
43	Peroxisome proliferator-activated receptor (PPAR)alpha expression in T cells mediates gender differences in development of T cell-mediated autoimmunity. *Journal of Experimental Medicine*, **2007**, 204, 321-30	16.6	139
42	Increased transcriptional activity of milk-related genes following the active phase of experimental autoimmune encephalomyelitis and multiple sclerosis. *Journal of Immunology*, **2007**, 179, 4074-82	5.3	16
41	Biological concepts of multiple sclerosis pathogenesis and relationship to treatment **2007**, 23-44		3
40	Peroxisome proliferator□activated receptor (PPAR)□expression in T cells mediates gender differences in development of T cell□mediated autoimmunity. *Journal of Cell Biology*, **2007**, 176, i9-i9	7.3	
39	Heterogeneity at the HLA-DRB1 locus and risk for multiple sclerosis. *Human Molecular Genetics*, **2006**, 15, 2813-24	5.6	246
38	Predictive modeling of therapy response in multiple sclerosis using gene expression data. *Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, **2006**, 2006, 5519-22		4

37	Systems-based medicine approaches to understand and treat complex diseases. The example of multiple sclerosis. *Autoimmunity*, **2006**, 39, 651-62	3	15
36	Genomics and new targets for multiple sclerosis. *Pharmacogenomics*, **2005**, 6, 151-61	2.6	8
35	10 Advanced data mining and predictive modelling at the core of personalised medicine. *Studies in Multidisciplinarity*, **2005**, 165-192		
34	Transcription-based prediction of response to IFNbeta using supervised computational methods. *PLoS Biology*, **2005**, 3, e2	9.7	122
33	Longitudinal analysis of B cell repertoire and antibody gene rearrangements during early HIV infection. *Genes and Immunity*, **2005**, 6, 66-9	4.4	3
32	Mapping gene activity in complex disorders: Integration of expression and genomic scans for multiple sclerosis. *Journal of Neuroimmunology*, **2005**, 167, 157-69	3.5	28
31	Modular transcriptional activity characterizes the initiation and progression of autoimmune encephalomyelitis. *Journal of Immunology*, **2005**, 174, 7412-22	5.3	33
30	Mapping multiple sclerosis susceptibility to the HLA-DR locus in African Americans. *American Journal of Human Genetics*, **2004**, 74, 160-7	11	274
29	Gene expression profiling in neurological disorders: toward a systems-level understanding of the brain. *NeuroMolecular Medicine*, **2004**, 6, 31-51	4.6	18
28	Pharmacogenomic analysis of interferon receptor polymorphisms in multiple sclerosis. *Genes and Immunity*, **2003**, 4, 147-52	4.4	68
27	Osteopontin polymorphisms and disease course in multiple sclerosis. *Genes and Immunity*, **2003**, 4, 312-5	4.4	52
26	Dynamic regulation of alternative ATP-binding cassette transporter A1 transcripts. *Biochemical and Biophysical Research Communications*, **2003**, 306, 463-8	3.4	13
25	Comment on "The influence of the proinflammatory cytokine, osteopontin, on autoimmune demyelinating disease". *Science*, **2003**, 299, 1845; author reply 1845	33.3	22
24	Direct deletion analysis in two Duchenne muscular dystrophy symptomatic females using polymorphic dinucleotide (CA)n loci within the dystrophin gene. *BMB Reports*, **2003**, 36, 179-84	5.5	6
23	Gene expression analysis reveals altered brain transcription of glutamate receptors and inflammatory genes in a patient with chronic focal (Rasmussen's) encephalitis. *Journal of Neuroimmunology*, **2002**, 128, 9-15	3.5	19
22	The HLA locus and multiple sclerosis in Spain. Role in disease susceptibility, clinical course and response to interferon-beta. *Journal of Neuroimmunology*, **2002**, 130, 194-201	3.5	68
21	Analysis of antibody gene rearrangement, usage, and specificity in chronic focal encephalitis. *Neurology*, **2002**, 58, 709-16	6.5	21
20	Large-scale gene-expression studies and the challenge of multiple sclerosis. *Genome Biology*, **2002**, 3, reviews1027	18.3	8

19	New insights into the genetics of multiple sclerosis. *Journal of Rehabilitation Research and Development*, **2002**, 39, 201-9		4
18	Multiple sclerosis: genomic rewards. *Journal of Neuroimmunology*, **2001**, 113, 171-84	3.5	111
17	The influence of the proinflammatory cytokine, osteopontin, on autoimmune demyelinating disease. *Science*, **2001**, 294, 1731-5	33.3	729
16	Transcriptional analysis of multiple sclerosis brain lesions reveals a complex pattern of cytokine expression. *Journal of Immunology*, **2000**, 165, 6576-82	5.3	134
15	B cell repertoire diversity and clonal expansion in multiple sclerosis brain lesions. *Journal of Immunology*, **1999**, 163, 5133-44	5.3	208
14	Carrier detection in Duchenne and Becker muscular dystrophy Argentine families. *Clinical Genetics*, **1998**, 54, 503-11	4	3
13	Deletion patterns in Argentine patients with Duchenne and Becker muscular dystrophy. *Neurological Research*, **1998**, 20, 409-414	2.7	5
12	A new point mutation (M313T) in the thyroid hormone receptor beta gene in a patient with resistance to thyroid hormone. *Thyroid*, **1997**, 7, 43-4	6.2	10
11	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum. *American Journal of Medical Genetics Part A*, **1997**, 70, 216-221		8
10	Four new polymorphisms in the human dystrophin gene from an Argentinian population. *Muscle and Nerve*, **1997**, 20, 1451-3	3.4	3
9	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum **1997**, 70, 216		1
8	Patient with an Xp21 contiguous gene deletion syndrome in association with agenesis of the corpus callosum. *American Journal of Medical Genetics Part A*, **1997**, 70, 216-21		2
7	The genetics of multiple sclerosis35-45		
6	Rephetio: Repurposing drugs on a hetnet [project]		3
5	Rephetio: Repurposing drugs on a hetnet [proposal]		2
4	Systematic integration of biomedical knowledge prioritizes drugs for repurposing		1
3	FutureMS Cohort Profile: A Scottish Multi-Centre Inception Cohort Study of Relapsing-Remitting Multiple Sclerosis		5
2	Progress Toward a Universal Biomedical Data Translator. *Clinical and Translational Science*,	4.9	1

1 Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. *Clinical and Translational Science*, 4·9 4